

Figure S1.

BjuA005498-BjPHL2a1	MY-SAIRSLPLDGGDYHGPLDGTNLPGDACLVLTTDPKPRLRWTAE LHERFVDAVTLGG	59
BjuB039462-BjPHL2b1	MYSAAIRSLPLD-GDYHGPLDGTNLPGDACLVLTTDPKPRLRWTAE LHERFVDAVTLGG	59
BjMYB1		0
BjuA012774-BjPHL2a	-MYSAIRSLPLDGGGEYHGPLDGTNLPGDACLVLTTDPKPRLRWTAE LHERFVEAVTELGG	59
BjuB032221-BjPHL2b	-MYSAIRSLALDGGGEYHGPLDGTNLPGDACLVLTTDPKPRLRWTAE LHEKFVEAVTELGG	59
BjuA005498-BjPHL2a1	PDKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKDSTDNS-KDASCVGESQDTGSS	118
BjuB039462-BjPHL2b1	PEKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTENS-KDASCVGESQDTGSS	118
BjMYB1		47
BjuA012774-BjPHL2a	PEKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTDNSNKDASCVGESQDTGSS	119
BjuB032221-BjPHL2b	PEKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTDNS-KDASCVGESQDTGSS	118
*****:*. * *****		
BjuA005498-BjPHL2a1	SSSSLRMAAQEQNEGYQVTEALRAQMEVQRRLEHQLVQRRQLR IEAQGKYLQSIL	178
BjuB039462-BjPHL2b1	SSSSLRMAAQEQNEGYQVTEALRAQMEVQRRLEHQLVQRRQLR IEAQGKYLQSIL	175
BjMYB1	SSSSLRMAAQEQNEGYQVTEALRAQMEVQRRLEHQLVQRRQLR IEAQGKYLQSIL	107
BjuA012774-BjPHL2a	SPSSLKLA AQEQNESYQVTEALRAQMEVQRRLEHQLVQRRQLVRIEAQGKYLQSIL	176
BjuB032221-BjPHL2b	SPSSLRLAAQEQNEGYQVTEALRAQMEVQRRLEHQLVQRRQLVRIEAQGKYLQSIL	175
* *: *****:***** *****:*****		
BjuA005498-BjPHL2a1	EKACKAFDDQAAAFVGLEAAREELSELAIKVSNSSQGT-AVPFFDTTKM-MMMPSLESEL	236
BjuB039462-BjPHL2b1	EKACQAFDDQAAAFVGLEAAREELSELAIKVS---QGT-AVPFLDATKM-MMMPSLSELE	230
BjMYB1	EKACQAFDDQAAAFVGLEAAREELSELAIKVS---QGT-AVPFLDATKM-MMMPSLSELE	162
BjuA012774-BjPHL2a	EKACKAFDEQAAMFTGLETAREELSELAIKVSNSSQGA-TVPFYDATKMMMMPSLSELE	235
BjuB032221-BjPHL2b	EKACKAFEEQAVTFGGLETAREELSDLAIKSSSSQGTTPVYF DATKMMMMPSLSELE	235
***:*. *. * *:*****:***. * *: :*:*. * *****		
BjuA005498-BjPHL2a1	VAV-DTK-NNITTNCVSSLTSNTNGSSVSAASMKKRLRGDDVGLGYEAGWNPSSSTI	294
BjuB039462-BjPHL2b1	VAI-DTK-NNITTNCVSSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	288
BjMYB1	VAI-DTK-NNITTNCVSSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	220
BjuA012774-BjPHL2a	VAAIDHKSNI TTNCVSSLTSNTNGSSVSAASMKKRHRGGD-NVGYEGSWTPGSTMG	294
BjuB032221-BjPHL2b	VAAIDQKSNIT-TNCVSSLTSNTNGSSVSAASMKKRHRG-D-SVGYEASWIMPSSTIG	292
** * * * ***** ** * . :***. * *:*		
BjuA005498-BjPHL2a1	G	295
BjuB039462-BjPHL2b1	-	288
BjMYB1	-	220
BjuA012774-BjPHL2a	-	294
BjuB032221-BjPHL2b	-	292

Figure S1. Multiple sequence alignment of BjPHL2 subclade members.

The protein sequences of all BjPHL2 subclade members are aligned with

Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The 71-amino acid-long deletion at the N-terminal and a YGQ insertion in the central between BjMYB1 and BjPHL2b1 are indicated in yellow box.

Figure S2.



BjMYB1	ACAAAGATGATGATGATGCCATCTTTGTCTGAGCTTGAAGTAGC	ATAGACACCAAAAAC 507
BjuB039462-BjPHL2b1	ACAAAGATGATGATGATGCCATCTTTGTCTGAGCTTGAAGTAGC	ATAGACACCAAAAAC 711
*****		
BjMYB1	AACATCACAACCAACTGTTTCGGTTGAAAGCTCTCTGACTTCCAACACCAATGGGAGCTCG	567
BjuB039462-BjPHL2b1	AACATCACAACCAACTGTTTCGGTTGAAAGCTCTCTGACTTCCAACACCAATGGGAGCTCG	771
*****		
BjMYB1	GTTTCTGCTGCATCGATGAAGAAGCGGCATCGTGGAGACGATGTAGGCCTAGGGTACGAG	627
BjuB039462-BjPHL2b1	GTTTCTGCTGCATCGATGAAGAAGCGGCATCGTGGAGACGATGTAGGCCTAGGGTACGAG	831
*****		
BjMYB1	GCAGGGTGGATTGTGCCTAGTAGTACCATTGGATAA	663
BjuB039462-BjPHL2b1	GCAGGGTGGATTGTGCCTAGTAGTACCATTGGA---	864
*****		

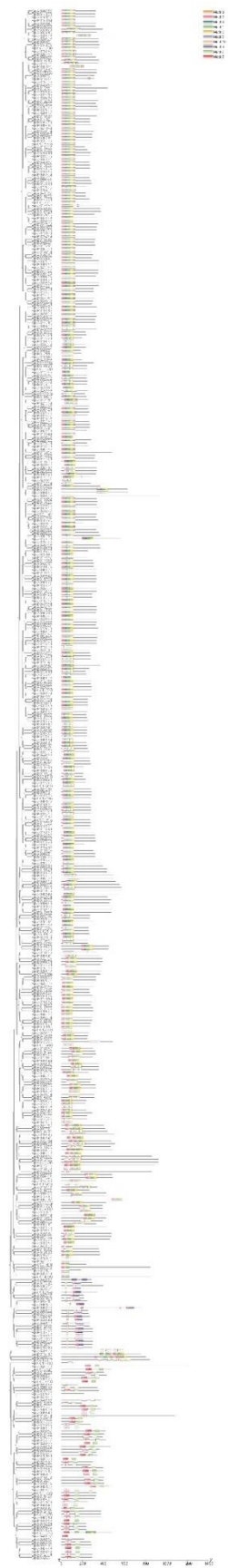
**Figure S2. Sequence alignment of BjMYB1 and BjPHL2b1 at the CDS level.** The CDS sequences of BjMYB1 and BjPHL2b1 are aligned with Clustal Omega. The observed 213 nt absence in the 5' end, 9 nt insertion in the central and a G to A replacement at 3' end between BjMYB1 and BjPHL2b1 are indicated by yellow box.

### Figure S3.

BjuB039462-BjPHL2b1	MYSAAIRSLPLDGDYHGFLDGTNLPGDACLVLTTDPKPRLRWTAE LHERFVDAVTQLGGP	60
BjMYB1		0
*****		
BjuB039462-BjPHL2b1	EKATPKTIMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTENSKDASCVGESQDTGSSSS	120
BjMYB1	MGVKGLTLYHLKSHLQKFRLGRQACKESTENSKDASCVGESQDTGSSSS	49
*****		
BjuB039462-BjPHL2b1	SSLRMAAQEQNEGYQVTEALRAQMEVQRRLHEQLE---VQRRLQLRIEAQGKYLQSILEK	177
BjMYB1	SSLRMAAQEQNEGYQVTEALRAQMEVQRRLHEQLEYGQVQRRLQLRIEAQGKYLQSILEK	109
*****		
BjuB039462-BjPHL2b1	ACQAFDDQAAAFVGLEAAREELSE LAIKVSQGTAVPFLDATKMMMP SLSELEVAIDTKN	237
BjMYB1	ACQAFDDQAAAFVGLEAAREELSE LAIKVSQGTAVPFLDATKMMMP SLSELEVAIDTKN	169
*****		
BjuB039462-BjPHL2b1	NITTNCSESSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	288
BjMYB1	NITTNCSESSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	220
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**Figure S3. Sequence alignment of BjMYB1 and BjPHL2b1 at the protein level.** The protein sequences of BjMYB1 and BjPHL2b1 are aligned with Clustal Omega. The observed 71-amino acid-long deletion at the N-terminal and a YGQ insertion in the central between BjMYB1 and BjPHL2b1 are indicated in yellow box.

Figure S4.



**Figure S4. Protein architecture of BjMYBs.** The distribution of conserved motifs identified from 502 BjMYB proteins are predicted using the MEME (Multiple Em for Motif Elicitation) tool. Each motif is represented by a number in colored box. See Table S2 for detailed motif information.